

SEQUENCE LISTING

SEQ ID NO: 1

SEQUENCE LENGTH: 1703

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL SEQUENCE: NO

ANTI-SENSE: NO

ORIGINAL SOURCE

ORGANISM: Gentiana triflora var. japonica

TISSUE TYPE: petal

IMMEDIATE SOURCE

LIBRARY: cDNA library

CLONE: PGAT4

SEQUENCE DESCRIPTION

TCATT ATG GAG CAA ATC CAA ATG GTG AAG GTT CTT GAA AAA TGC CAA 47

Met Glu Gln Ile Gln Met Val Lys Val Leu Glu Lys Cys Gln

-1 1 5 10

GTT ACA CCA CCA TCT GAC ACA ACA GAT GTC GAG TTA TCG CTA CCG GTA 95

Val Thr Pro Pro Ser Asp Thr Thr Asp Val Glu Leu Ser Leu Pro Val

15 20 25

ACA TTC TTC GAT ATC CCC TGG TTG CAC TTG AAT AAG ATG CAG TCC CTT 143

Thr Phe Phe Asp Ile Pro Trp Leu His Leu Asn Lys Met Gln Ser Leu

30 35 40 45

CTG TTT TAC GAC TTT CCG TAC CCA AGA ACA CAT TTC TTG GAC ACT GTT 191

Leu Phe Tyr Asp Phe Pro Tyr Pro Arg Thr His Phe Leu Asp Thr Val

50 55 60

ATC CCT AAT CTT AAG GCC TCT TTG TCT CTC ACT CTA AAA CAC TAC GTT 239

Ile Pro Asn Leu Lys Ala Ser Leu Ser Leu Thr Leu Lys His Tyr Val

65 70 75

CGG CTT AGC GGA AAT TTG TTG ATG CCG ATC AAA TCG GGC GAA ATG CCG 287

Pro Leu Ser Gly Asn Leu Leu Met Pro Ile Lys Ser Gly Glu Met Pro

80 85 90

AAG TTT CAG TAC TCC CGT GAT GAG GGC GAC TCG ATA ACT TTG ATC GTT 335

Lys Phe Gln Tyr Ser Arg Asp Glu Gly Asp Ser Ile Thr Leu Ile Val

95 100 105

GCG GAG TCT GAC CAG GAT TTT GAC TAC CTT AAA GGT CAT CAA CTG GTA 383  
Ala Glu Ser Asp Gln Asp Phe Asp Tyr Leu Lys Gly His Gln Leu Val  
110 115 120 125  
GAT TCC AAT GAT TTG CAT GGC CTT TTT TAT GTT ATG CCA CGG GTT ATA 431  
Asp Ser Asn Asp Leu His Gly Leu Phe Tyr Val Met Pro Arg Val Ile  
130 135 140  
AGG ACC ATG CAA GAC TAT AAA GTG ATC CCG CTC GTA GCC GTG CAA GTA 479  
Arg Thr Met Gln Asp Tyr Lys Val Ile Pro Leu Val Ala Val Gln Val  
145 150 155  
ACC GTT TTT CCT AAC CGT GGC ATA GCC GTG GCT CTG ACG GCA CAT CAT 527  
Thr Val Phe Pro Asn Arg Gly Ile Ala Val Ala Leu Thr Ala His His  
160 165 170  
TCA ATT GCA GAT CCT AAA AGT TTT GTA ATG TTC ATC AAT GCT TGG GCC 575  
Ser Ile Ala Asp Ala Lys Ser Phe Val Met Phe Ile Asn Ala Trp Ala  
175 180 185  
TAT ATT AAC AAA TTT GGG AAA GAC GCG GAC TTG TTG TCC GCG AAT CTT 623  
Tyr Ile Asn Lys Phe Gly Lys Asp Ala Asp Leu Leu Ser Ala Asn Leu  
190 195 200 205  
CTT CCA TCT TTC GAT AGA TCG ATA ATC AAA GAT CTG TAT GCC CTA GAG 671  
Leu Pro Ser Phe Asp Arg Ser Ile Ile Lys Asp Leu Tyr Gly Leu Glu  
210 215 220  
GAA ACA TTT TGG AAC GAA ATG CAA GAT GTT CTT GAA ATG TTC TCT AGA 719  
Glu Thr Phe Trp Asn Glu Met Gln Asp Val Leu Glu Met Phe Ser Arg  
225 230 235  
TTT GGA AGC AAA CCC CCT CGA TTC AAC AAG GTA CGA GCT ACA TAT GTC 767  
Phe Gly Ser Lys Pro Pro Arg Phe Asn Lys Val Arg Ala Thr Tyr Val  
240 245 250  
CTC TCC CTT GCT GAA ATC CAG AAG CTA AAG AAC AAA GTA CTG AAT CTC 815  
Leu Ser Leu Ala Glu Ile Gln Lys Leu Lys Asn Lys Val Leu Asn Leu  
255 260 265  
AGA GGA TCC GAA CCG ACA ATA CGT GTA ACG ACG TTC ACA ATG ACG TGT 863  
Arg Gly Ser Glu Pro Thr Ile Arg Val Thr Thr Phe Thr Met Thr Cys  
270 275 280 285  
GGA TAC GTA TGG ACA TGC ATG GTC AAA TCA AAA GAT GAC GTC GTA TCA 911  
Gly Tyr Val Trp Thr Cys Met Val Lys Ser Lys Asp Asp Val Val Ser  
290 295 300

GAG GAA TCA TCG AAC GAC GAA AAT GAG CTC GAG TAC TTC AGT TTT ACA	959		
Glu Glu Ser Ser Asn Asp Glu Asn Glu Leu Glu Tyr Phe Ser Phe Thr			
305	310	315	
GCG GAT TGC CGA GGA CTT CTG ACG CCC CCG TGT CCG CCT AAC TAC TTT	1007		
Ala Asp Cys Arg Gly Leu Leu Thr Pro Pro Cys Pro Pro Asn Tyr Phe			
320	325	330	
GGC AAC TGT CTT GCG TCA TGC GTT GCA AAA GCA ACA CAT AAA GAG TTA	1055		
Gly Asn Cys Leu Ala Ser Cys Val Ala Lys Ala Thr His Lys Glu Leu			
335	340	345	
GTT GGG GAT AAA GGG CTT CTT GTT GCA GTT GCA GCT ATT GGA GAA GCC	1103		
Val Gly Asp Lys Gly Leu Leu Val Ala Val Ala Ala Ile Gly Glu Ala			
350	355	360	365
ATT CAA AAG AGG TTG CAC AAC GAA AAA GGC GTT CTT GCA GAT GCA AAA	1151		
Ile Glu Lys Arg Leu His Asn Glu Lys Gly Val Leu Ala Asp Ala Lys			
370	375	380	
ACT TGG TTA TCG GAA TCT AAT GGA ATC CCT TCA AAA AGA TTT CTC GGG	1199		
Thr Trp Leu Ser Glu Ser Asn Gly Ile Pro Ser Lys Arg Phe Leu Gly			
385	390	395	
ATT ACC GGA TCG CCT AAG TTC CAT TCG TAT GGT GTA GAT TTT GGA TGG	1247		
Ile Thr Gly Ser Pro Lys Phe Asp Ser Tyr Gly Val Asp Phe Gly Trp			
400	405	410	
GGA AAG CCT GCA AAA TTT GAC ATT ACC TCT GTT GAT TAT GCA GAA TTG	1295		
Gly Lys Pro Ala Lys Phe Asp Ile Thr Ser Val Asp Tyr Ala Glu Leu			
415	420	425	
ATT TAT GTG ATT CAG TCC AGG GAT TTT GAA AAA GGT GTG GAG ATT GGA	1343		
Ile Tyr Val Ile Gln Ser Arg Asp Phe Glu Lys Gly Val Glu Ile Gly			
430	435	440	445
GTA TCA TTG CCT AAG ATT CAT ATG GAT GCA TTT GCA AAA ATC TTT GAA	1391		
Val Ser Leu Pro Lys Ile His Met Asp Ala Phe Ala Lys Ile Phe Glu			
450	455	460	
GAA GGC TTT TGC TCT TTG TCA TAGTCTCTTT AATAGAACCA TATTTGCTGC	1442		
Glu Gly Phe Cys Ser Leu Ser			
465	468		
AATAAAAGTAC CAAGTCCTTT AGTAACACTA CACCAAACCC TACTTCGAG GCGGGAACAC	1502		
CACAAACGAGG TTCAATCACT AGAAGGTTGT ACTTCATAAA TTCCAGAGGT CGAATATACA	1562		
CCGTTGTCCT CTGAAAAGTT GAACCTCACCA CCTGACATGG TGTTACGATA GGTATTGTAT	1622		
AATGCCATTA TATACTTCCA TAAAGTATCC TATGCAATAG AGAACATGTT ATGTGTTAAA	1682		

AAAAAAAAAA AAAAAAAA A

1703

SEQ ID NO: 2

SEQUENCE LENGTH: 1622

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL SEQUENCE: No

ANTI-SENSE: No

ORIGINAL SOURCE

ORGANISM: Gentiana triflora var. japonica

TISSUE TYPE: petal

IMMEDIATE SOURCE

LIBRARY: cDNA library

CLONE: pGAT106

SEQUENCE DESCRIPTION

GAACCATTGA ATCCAATTAA TCTGATTAT TAAG ATG GCA GGA AAT TCC GAG

52

Met Ala Gly Asn Ser Glu

1

5

GAT ATC AAA GTT CTT GAG AAA TGC CGT GTT GCG CCA CCA CCG GAC GCC

100

Asp Ile Lys Val Leu Glu Lys Cys Arg Val Ala Pro Pro Pro Asp Ala

10

15

20

GTC GCC GAG TTT ACA GTC CCA CTG TCG TTT TTC GAC ATG CGA TGG TTG

148

Val Ala Glu Phe Thr Val Pro Leu Ser Phe Phe Asp Met Arg Trp Leu

25

30

35

ATC TCT GAT GCA GAA CAC CAT CTG CAT TTC TAC AGA TTC CGC CAT CCT

196

Ile Ser Asp Ala Glu His His Leu His Phe Tyr Arg Phe Arg His Pro

40

45

50

TGT CCC AAC TCT AAA TTT ATC ATT TCA TCC ATT AAA TCG TCC CTT TCC

244

Cys Pro Asn Ser Lys Phe Ile Ile Ser Ser Ile Lys Ser Ser Leu Ser

55

60

65

70

CTT GTT CTC AAA CAC TTT CTT CCG TTA GCC GGG AAT TTG ATT TGG CCG

292

Leu Val Leu Lys His Phe Leu Pro Leu Ala Gly Asn Leu Ile Trp Pro

75

80

85

GTA GAT TCC TCC GAT AGA ATG CCG GAG TTG CGT TAC AAG AAA GGG GAC

340

Val Asp Ser Ser Asp Arg Met Pro Glu Leu Arg Tyr Lys Lys Gly Asp

90

95

100

TCC	GTT	TCT	TTA	ACA	ATT	GCA	GAA	TCG	AGC	ATG	GAT	TTT	GAT	TAT	CTC	388
Ser	Val	Ser	Leu	Thr	Ile	Ala	Glu	Ser	Ser	Met	Asp	Phe	Asp	Tyr	Leu	
105														115		
GCC	GGA	GAT	CAT	CAG	AGG	GAT	TCT	TAT	AAA	TTC	AAC	GAT	TTG	ATT	CCG	436
Ala	Gly	Asp	His	Gln	Arg	Asp	Ser	Tyr	Lys	Phe	Asn	Asp	Leu	Ile	Pro	
120													130			
CAG	CTG	CCA	GAA	CCG	ATT	GTA	ACC	TCC	GGC	GAC	GAA	GTA	TTA	CCA	CTT	484
Gln	Leu	Pro	Glu	Pro	Ile	Val	Thr	Ser	Gly	Asp	Glu	Val	Leu	Pro	Leu	
135													145		150	
TTT	GCT	TTA	CAG	GTG	ACG	GTG	TTC	TCC	AAC	ACC	GGT	ATA	TGC	ATT	GGA	532
Phe	Ala	Leu	Gln	Val	Thr	Val	Phe	Ser	Asn	Thr	Gly	Ile	Cys	Ile	Gly	
155												160		165		
CGC	AAT	CTT	CAT	CAA	GTT	CTT	GGT	GAT	GCC	AGT	TCT	TTT	CTG	CAT	TTT	580
Arg	Asn	Leu	His	Gln	Val	Leu	Gly	Asp	Ala	Ser	Ser	Phe	Leu	His	Phe	
170												175		180		
AAT	AAA	TTA	TGG	GTT	TTG	GTT	GAC	AAA	TCC	AAT	GGA	GAT	TCA	TTA	AAG	628
Asn	Lys	Leu	Trp	Val	Leu	Val	Asp	Lys	Ser	Asn	Gly	Asp	Ser	Leu	Lys	
185												190		195		
TTC	CTT	CCA	CTT	TCT	TCT	CTA	CCT	ATG	TAC	GAC	AGA	TCT	GTG	GTG	CAA	676
Phe	Leu	Pro	Leu	Ser	Ser	Leu	Pro	Met	Tyr	Asp	Arg	Ser	Val	Val	Gln	
200												205		210		
GAT	CCA	TTT	CAT	ATT	CGT	CGA	AAA	ATC	TAC	AAT	GAA	AGA	AAA	CTG	CTC	724
Asp	Pro	Phe	His	Ile	Arg	Arg	Lys	Leu	Tyr	Asn	Glu	Arg	Lys	Leu	Leu	
215												220		225		230
AAA	TCT	CAG	GGC	ACA	CCT	ACT	GTT	CTA	AAT	CCA	GCA	ATT	TCT	AAA	GAT	772
Lys	Ser	Gln	Gly	Thr	Pro	Thr	Val	Leu	Asn	Pro	Ala	Ile	Ser	Lys	Asp	
235												240		245		
GAA	GTT	CGA	GCC	ACC	TTC	ATC	CTA	CAC	CCT	ATT	GAT	ATC	ATG	AAG	CTC	820
Glu	Val	Arg	Ala	Thr	Phe	Ile	Leu	His	Pro	Ile	Asp	Ile	Met	Lys	Leu	
250												255		260		
AAG	AAA	TTC	ATT	TCG	TCA	AAA	AAT	CGC	AAC	TTA	ACC	GGT	AGT	AGT	AAT	868
Lys	Lys	Phe	Ile	Ser	Ser	Lys	Asn	Arg	Asn	Leu	Thr	Gly	Ser	Ser	Asn	
265												270		275		
TAT	AAT	CTG	TCA	ACT	TTC	ACG	GTG	ACA	TCT	GCA	CTG	ATC	TGG	ACA	TGC	916
Tyr	Asn	Leu	Ser	Thr	Phe	Thr	Val	Thr	Ser	Ala	Leu	Ile	Trp	Thr	Cys	
280												285		290		

TTG TCG AAA TCA TTA GAC ACC GTC GTA AGA GAG AAG GTG GAA GAG GAT 964  
Leu Ser Lys Ser Leu Asp Thr Val Val Arg Glu Lys Val Glu Glu Asp  
295 300 305 310  
AAA CAT GCA GCA AAC TTA TGT GCT TTC ATC AAC TGC CGA CAA CGT TTT 1012  
Lys His Ala Ala Asn Leu Cys Ala Phe Ile Asn Cys Arg Gln Arg Phe  
315 320 325  
GCT CCG CCG ATA CCT CAA AAT TAC TTT GGA AAT TGC ATA GTG CCT TGT 1060  
Ala Pro Pro Ile Pro Gln Asn Tyr Phe Gly Asn Cys Ile Val Pro Cys  
330 335 340  
ATG GTG GGA TCG ACT CAT GAG CAA CTT GTA GGA AAT GAA GGG TTG TCG 1108  
Met Val Gly Ser Thr His Glu Gln Leu Val Gly Asn Glu Gly Leu Ser  
345 350 355  
GTA GCT GCA ACC GCC ATC GGA GAT GCT ATC CAT AAG AGG TTA CAT GAC 1156  
Val Ala Ala Thr Ala Ile Gly Asp Ala Ile His Lys Arg Leu His Asp  
360 365 370  
TAC GAA GGA ATT CTG AGA GGA GAT TGG ATA TCG CCG CCC CGA TCA ACA 1204  
Tyr Glu Gly Ile Leu Arg Gly Asp Trp Ile Ser Pro Pro Arg Ser Thr  
375 380 385 390  
TCT GCG GCA CCA AGG TCG ACG CTC ATT TAT GTC GTT GGA TCC GCA CAA 1252  
Ser Ala Ala Pro Arg Ser Thr Leu Ile Tyr Val Val Gly Ser Ala Gln  
395 400 405  
CGC AAT GTG CAT GAT TTT GAT GCA GAT TTT GGT TGG GGA AAG CTT GAA 1300  
Arg Asn Val His Asp Phe Asp Ala Asp Phe Gly Trp Gly Lys Leu Glu  
410 415 420  
AAG CAT GAA TCT GTT TCA ACT AAT CCT TCG GCA ACA CTA ATT TTG ATC 1348  
Lys His Glu Ser Val Ser Thr Asp Pro Ser Ala Thr Leu Ile Leu Ile  
425 430 435  
TCT CGG TCC AGA AGA TTT AAA GGA GCA CTT GAG CTT GGC ATT TCT TTG 1396  
Ser Arg Ser Arg Arg Phe Lys Gly Ala Leu Glu Leu Gly Ile Ser Leu  
440 445 450  
CCT AAG AAT AGG ATG GAC GCA TTT GCC ACC ATT TTT ACG AAT TTC ATC 1444  
Pro Lys Asn Arg Met Asp Ala Phe Ala Thr Ile Phe Thr Asn Phe Ile  
455 460 465 470  
AAT AGT CTC CAT GTG AGG AGC CCT TTG TAAGAAAAAA GTGGTATCAA 1491  
Asn Ser Leu His Val Arg Ser Pro Leu  
475 479  
TGTATAAAAAA AGACAGACAA GTTATGATGC AACAAATGTT TTAGGAGATT ACAAAATCCAT 1551

GGGAAGATGT ATCAAACCTCA TCTCTCTATA TATATATATT CAATTGTTTT AAAAAAAAAA 1611  
AAAAAAAAAA A 1622

SEQ ID NO: 3

SEQUENCE LENGTH: 1605

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL SEQUENCE: No

ANTI-SENSE: No

ORIGINAL SOURCE

ORGANISM: Petunia hybrida

TISSUE TYPE: petal

IMMEDIATE SOURCE

LIBRARY: cDNA library

CLONE: pPAT48

SEQUENCE DESCRIPTION

TGTCGACGAA ATCCATTCA TTTCCTCTTC TTTCTTGT TTCTAATTTC GTCATCATTG 60  
TTATCC ATG GCA GGT GAA GTA GCA AAA CAA GAA GTT ACA AAA GTG AAA 108  
Met Ala Gly Glu Val Ala Lys Gln Glu Val Thr Lys Val Lys  
1 5 10  
GTC CTG AAA AAA ACA AAC GTG AAA CCA CAT AAA CCA CTA GGA AAA AAA 156  
Val Leu Lys Lys Thr Asn Val Lys Pro His Lys Pro Leu Gly Lys Lys  
15 20 25 30  
GAG TGT CAA TTG GTA ACA TTT GAT CTT CCT TAC CTA GCT TTC TAT TAC 204  
Glu Cys Gln Leu Val Thr Phe Asp Leu Pro Tyr Leu Ala Phe Tyr Tyr  
35 40 45  
AAC CAA AAA TTT CTC ATC TAT AAA GGT GCT GAA AAC TTT GAC GAG ACG 252  
Asn Gln Lys Phe Leu Ile Tyr Lys Gly Ala Glu Asn Phe Asp Glu Thr  
50 55 60  
GTG GAA AAA ATT AAA GAT GGA CTG GCC TTA GTA TTG GTG GAT TTC TAT 300  
Val Glu Lys Ile Lys Asp Gly Leu Ala Leu Val Leu Val Asp Phe Tyr  
65 70 75  
CAA CTA GCT GGG AAA CTT GGA AAA GAT GAA GAA GGG GTT TTC AGG GTG 348  
Gln Leu Ala Gly Lys Leu Gly Lys Asp Glu Glu Gly Val Phe Arg Val  
80 85 90

GAA TAC GAC GAT GAC ATG GAT GGT GTA GAG GTG ACA GTG GCT GTT GCA 396  
Glu Tyr Asp Asp Asp Met Asp Gly Val Glu Val Thr Val Ala Val Ala  
95 100 105 110  
GAA GAG ATA GAA GTT GCA GAT CTT ACT GAT GAA GAA GGC ACC ACC AAA 444  
Glu Glu Ile Glu Val Ala Asp Leu Thr Asp Glu Glu Gly Thr Thr Lys  
115 120 125  
TTC CAG GAC TTG ATT CCT TGT AAT AAA ATC TTG AAT TTG GAA GGG CTT 492  
Phe Gln Asp Leu Ile Pro Cys Asn Lys Ile Leu Asn Leu Glu Gly Leu  
130 135 140  
CAT CGC CCT CTT CTA GCT GTG CAG CTC ACC AAG CTC AAG GAC GGG CTC 540  
His Arg Pro Leu Leu Ala Val Gln Leu Thr Lys Leu Lys Asp Gly Leu  
145 150 155  
ACC ATG GGA TTA GCA TTT AAC CAT GCT GTG CTG GAT GGT ACT TCG ACG 588  
Thr Met Gly Leu Ala Phe Asn His Ala Val Leu Asp Gly Thr Ser Thr  
160 165 170  
TGG CAC TTT ATG ACC TCG TGG TCC GAG CTT TGC TGT GGG TCC ACC TCA 636  
Trp His Phe Met Thr Ser Trp Ser Glu Leu Cys Cys Gly Ser Thr Ser  
175 180 185 190  
ATT TCT GTC CCA CCA TTC CTT GAA CGA ACC AAG GCT CGT AAC ACT CGA 684  
Ile Ser Val Pro Pro Phe Leu Glu Arg Thr Lys Ala Arg Asn Thr Arg  
195 200 205  
GTC AAG CTC AAC CTC TCT CAA CCA TCA GAT GCA CCC GAA CAT GCT AAG 732  
Val Lys Leu Asn Leu Ser Gln Pro Ser Asp Ala Pro Glu His Ala Lys  
210 215 220  
TCA GCA ACC AAC GGT GAT GTC CCG GCC AAC GTA GAC CCA CCT CTT CGC 780  
Ser Ala Thr Asn Gly Asp Val Pro Ala Asn Val Asp Pro Pro Leu Arg  
225 230 235  
GAA AGA GTA TTC AAG TTC TCC GAG TTA GCA ATT GAC AAA ATC AAG TCA 828  
Glu Arg Val Phe Lys Phe Ser Glu Leu Ala Ile Asp Lys Ile Lys Ser  
240 245 250  
ACA GTC AAT GCC AAC TCA GGA GAG ACC CCA TTC TCC ACA TTC CAA TCA 876  
Thr Val Asn Ala Asn Ser Gly Glu Thr Pro Phe Ser Thr Phe Gln Ser  
255 260 265 270  
CTC TCC GCA CAC GTG TGG CTA GCC GTC ACA CGT GCG CGC CAA CTC AAG 924  
Leu Ser Ala His Val Trp Leu Ala Val Thr Arg Ala Arg Gln Leu Lys  
275 280 285

CCC GAG GAC TAC ACT GTG TAC ACT GTG TTT GCT GAT TGC AGG AAA AGG	972
Pro Glu Asp Tyr Thr Val Tyr Thr Val Phe Ala Asp Cys Arg Lys Arg	
290 295 300	
GTT GAT CCT CCA ATG CCA GAA AGT TAC TTC GGC AAC CTA ATT CAG GCA	1020
Val Asp Pro Pro Met Pro Glu Ser Tyr Phe Gly Asn Leu Ile Gln Ala	
305 310 315	
ATT TTC ACA GTG ACC GCG GCA GGT TTG TTA CTA GCA AGC CCG ATC GAG	1068
Ile Phe Thr Val Thr Ala Ala Gly Leu Leu Leu Ala Ser Pro Ile Glu	
320 325 330	
TTC GCT GGT GGG ATG ATA CAA CAA GCG ATC GTG AAG CAT GAC GCT AAG	1116
Phe Ala Gly Gly Met Ile Gln Gln Ala Ile Val Lys His Asp Ala Lys	
335 340 345 350	
GCC ATT GAT CAA AGA AAC AAG GAG TGG GAG AGC AAC CCG AAG ATC TTT	1164
Ala Ile Asp Glu Arg Asn Lys Glu Trp Glu Ser Asn Pro Lys Ile Phe	
355 360 365	
CAG TAC AAA GAT GCT GGA GTG AAC TGT GTT GCT GTT GGA AGT TCG CCA	1212
Gln Tyr Lys Asp Ala Gly Val Asn Cys Val Ala Val Gly Ser Ser Pro	
370 375 380	
AGG TTC AAG GTT TAC GAC GTG GAT TTT GGA TGG GGA AAG CCA GAG AGT	1260
Arg Phe Lys Val Tyr Asp Val Asp Phe Gly Trp Gly Lys Pro Glu Ser	
385 390 395	
G TG AGG AGT GGT TCG AAC AAT AGG TTT GAT GGA ATG GTG TAT TTG TAC	1308
Val Arg Ser Gly Ser Asn Asn Arg Phe Asp Gly Met Val Tyr Leu Tyr	
400 405 410	
CAA GGC AAA AAT GGA GGA AGA AGC ATT GAT GTG GAG ATT AGT TTG GAA	1356
Gln Gly Lys Asn Gly Gly Arg Ser Ile Asp Val Glu Ile Ser Leu Glu	
415 420 425 430	
GCA AAT GCT ATG GAG AGG TTG GAG AAA GAT AAA GAG TTC CTC ATG GAA	1404
Ala Asn Ala Met Glu Arg Leu Glu Lys Asp Lys Glu Phe Leu Met Glu	
435 440 445	
ACT GCT TAATTTGCTT AGCTTGGACT CAACTGGCTA CACTTTATTT ATGAGCTGCT	1460
Thr Ala	
ATGACTGACA TGCATGTATG TTTATTTTT TTGGAGGGT TCTTCCCTT TATTGTTTC	1520
TATGTTTTT CTTCTTGTA CGTTATGAAG AGAAACCGAG TATAAAGGAA TAATGTTTC	1580
AGTTATTAAA AAAAAAAA AAAAA	1605

SEQ ID NO: 4

SEQUENCE LENGTH: 1479

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL SEQUENCE: No

ANTI-SENSE: No

ORIGINAL SOURCE

ORGANISM: *Perilla ocimoides*

TISSUE TYPE: leaf

IMMEDIATE SOURCE

LIBRARY: cDNA library

CLONE: pSAT208

SEQUENCE DESCRIPTION

CC GTG ATC GAA ACG TGT AGA GTT GGG CCG CCG CCG GAC TCG GTG GCG	47
Val Ile Glu Thr Cys Arg Val Gly Pro Pro Pro Asp Ser Val Ala	
1 5 10 15	
GAG CAA TCG GTG CCG CTC ACA TTC TTC GAC ATG ACG TGG CTG CAT TTT	95
Glu Gln Ser Val Pro Leu Thr Phe Phe Asp Met Thr Trp Leu His Phe	
20 25 30	
CAT CCC ATG CTT CAG CTC CTC TTC TAC GAA TTC CCT TGT TCC AAG CAA	143
His Pro Met Leu Gln Leu Leu Phe Tyr Glu Phe Pro Cys Ser Lys Gln	
35 40 45	
CAT TTT TCA GAA TCC ATC GTT CCA AAA CTC AAA CAA TCT CTC TCT AAA	191
His Phe Ser Glu Ser Ile Val Pro Lys Leu Lys Gln Ser Leu Ser Lys	
50 55 60	
ACT CTC ATA CAC TTC TTC CCT CTC TCA TGC AAT TTA ATC TAC CCT TCA	239
Thr Leu Ile His Phe Phe Pro Leu Ser Cys Asn Leu Ile Tyr Pro Ser	
65 70 75	
TCC CCG GAG AAA ATG CCG GAG TTT CCG TAT CTA TCC GGG GAC TCG GTT	287
Ser Pro Glu Lys Met Pro Glu Phe Arg Tyr Leu Ser Gly Asp Ser Val	
80 85 90 95	
TCT TTC ACC ATC GCA GAA TCT AGC GAC GAC TTC GAT GAT CTC GTC GGA	335
Ser Phe Thr Ile Ala Glu Ser Ser Asp Asp Phe Asp Asp Leu Val Gly	
100 105 110	
AAT CGT CCA GAA TCT CCC GTT AGG CTC TAC AAC TTT GTC CCT AAA TTG	383
Asn Arg Pro Glu Ser Pro Val Arg Leu Tyr Asn Phe Val Pro Lys Leu	
115 120 125	

CCG CCC ATT GTC GAA GAA TCC GAT AGA AAA CTC TTC CAA GTT TTC GCC 431  
Pro Pro Ile Val Glu Glu Ser Asp Arg Lys Leu Phe Gln Val Phe Ala  
130 135 140  
GTG CAG GTG ACT CTT TTC CCA GGC CGA GGC GTC GGT ATT GGA ATA GCA 479  
Val Gln Val Thr Leu Phe Pro Gly Arg Gly Val Gly Ile Gly Ile Ala  
145 150 155  
ACG CAT CAC ACC GTT AGC GAC GCC CCG TCG TTT CTC GCG TTT ATA ACG 527  
Thr His His Thr Val Ser Asp Ala Pro Ser Phe Ile Ala Phe Ile Thr  
160 165 170 175  
GCT TGG TCT TCA ATG AGC AAA CAC ATT GAA AAT GAA GAT GAA GAT GAA 575  
Ala Trp Ser Ser Met Ser Lys His Ile Glu Asn Glu Asp Glu Asp Glu  
180 185 190  
GAA TTT AAA TCT TTG CCA GTT TTC GAT AGA TCC GTC ATA AAA TAT CCG 623  
Glu Phe Lys Ser Leu Pro Val Phe Asp Arg Ser Val Ile Lys Tyr Pro  
195 200 205  
ACG AAA TTT GAC TCC ATT TAT TGG AGA AAC GCG CTA AAA TTT CCT TTG 671  
Thr Lys Phe Asp Ser Ile Tyr Trp Arg Asn Ala Leu Lys Phe Pro Leu  
210 215 220  
CAA TCT CGT CAT CCC TCA TTA CCG ACG GAC CGC ATT CGA ACC ACG TTC 719  
Gln Ser Arg His Pro Ser Ile Pro Thr Asp Arg Ile Arg Thr Thr Phe  
225 230 235  
GTT TTC ACC CAA TCC AAA ATT AAG AAA TTG AAG GGT TGG ATT CAG TCC 767  
Val Phe Thr Gln Ser Lys Ile Lys Lys Leu Lys Gly Trp Ile Gln Ser  
240 245 250 255  
AGA GTT CCA AGT TTA GTC CAT CTC TCA TCT TTT GTA GCG ATT GCA GCT 815  
Arg Val Pro Ser Leu Val His Leu Ser Ser Phe Val Ala Ile Ala Ala  
260 265 270  
TAT ATG TGG GCT GGC ATA ACG AAA TCA TTC ACA GCA GAT GAA GAC CAA 863  
Tyr Met Trp Ala Gly Ile Thr Lys Ser Phe Thr Ala Asp Glu Asp Gln  
275 280 285  
GAC AAC GAG GAT GCA TTT TTC TTG ATT CCG GTC GAT CTA AGG CCA CGA 911  
Asp Asn Glu Asp Ala Phe Phe Leu Ile Pro Val Asp Leu Arg Pro Arg  
290 295 300  
TTA GAT CCG CCG GTT CCT GAA AAT TAC TTC GGG AAC TGC TTA TCG TAC 959  
Leu Asp Pro Pro Val Pro Glu Asn Tyr Phe Gly Asn Cys Leu Ser Tyr  
305 310 315

GGC CTG CCG AGA ATG CGG CGG CGA GAG CTG GTG GGA GAG AAA GGG GTG 1007  
Ala Leu Pro Arg Met Arg Arg Arg Glu Leu Val Gly Glu Lys Gly Val  
320 325 330 335  
TTT CTG GCA GCT GAG GTA ATC GCG GCG GAG ATA AAA AAA AGG ATC AAC 1055  
Phe Leu Ala Ala Glu Val Ile Ala Ala Glu Ile Lys Lys Arg Ile Asn  
340 345 350  
GAC AAG AGA ATA TTA GAA ACG GTG GAG AAA TGG TCG CCG GAG ATT CGT 1103  
Asp Lys Arg Ile Leu Glu Thr Val Glu Lys Trp Ser Pro Glu Ile Arg  
355 360 365  
AAA GCG TTG CAG AAA TCA TAT TTT TCG GTG GCA GGA TCG AGC AAG CTA 1151  
Lys Ala Leu Gln Lys Ser Tyr Phe Ser Val Ala Gly Ser Ser Lys Leu  
370 375 380  
GAT CTT TAC GGT GCA GAT TTT GGA TGG GGG AAG GCG AGA AAG CAA GAA 1199  
Asp Leu Tyr Gly Ala Asp Phe Gly Trp Gly Lys Ala Arg Lys Gln Glu  
385 390 395  
ATA TTG TCG ATT GAT GGG GAG AAA TAT GCA ATG ACR CTT TGT AAA GCC 1247  
Ile Leu Ser Ile Asp Gly Glu Lys Tyr Ala Met Thr Leu Cys Lys Ala  
400 405 410 415  
AGG GAT TTC GAA GGA GGA TTG GAG GTT TGC TTG TCT TTG CCT AAG GAC 1295  
Arg Asp Phe Glu Gly Leu Glu Val Cys Leu Ser Leu Pro Lys Asp  
420 425 430  
AAA ATG GAT GCT TTT GCT GCT TAT TTT TCA CTG GGA ATT AAT GGT 1340  
Lys Met Asp Ala Phe Ala Ala Tyr Phe Ser Leu Gly Ile Asn Gly  
435 440 446  
TAATAATGT ATGTAATTAA ACTAATATTA TTATGTAACA ATTAATTAAG TGTTGAGTAA 1400  
CGTGAAGAAT AATCCCTATT ATATATTAT GATTTGGTTC AAATAAAGTG TAAAGCCTCT 1460  
TGAAAAAAA AAAAAAAA 1479

SEQ ID NO: 5

SEQUENCE LENGTH: 1508

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL SEQUENCE: No

ANTI-SENSE: No

ORIGINAL SOURCE

ORGANISM: Senecio cruentus

TISSUE TYPE: petal  
IMMEDIATE SOURCE

LIBRARY: cDNA library

CLONE: pCAT8

SEQUENCE DESCRIPTION

TG AAC ATT CTC GAA CAT GCC CGA ATA TCG GCC CCC TCG GGC ACC ATC	47
Asn Ile Leu Glu His Ala Arg Ile Ser Ala Pro Ser Gly Thr Ile	
1 5 10 15	
GGC CAT CGC TCG TTA TCT CTT ACT TTC TTC GAC ATT ACT TGG CTA CTC	95
Gly His Arg Ser Leu Ser Leu Thr Phe Phe Asp Ile Thr Trp Leu Leu	
20 25 30	
TTC CCT CCG GTC CAC CAT CTT TTC TAT GAC TTT CCA CAT TCT AAA	143
Phe Pro Pro Val His His Leu Phe Phe Tyr Asp Phe Pro His Ser Lys	
35 40 45	
TCC CAT TTC ATG GAC ACT ATT GTT CCC AGG CTA AAA CAA TCT TTA TCG	191
Ser His Phe Met Asp Thr Ile Val Pro Arg Leu Lys Gln Ser Leu Ser	
50 55 60	
GTC ACT CTT CAA CAT TTT TTC ECG TTT GCT AGT AAT TTG ATT GTA TTT	239
Val Thr Leu Gln His Phe Phe Pro Phe Ala Ser Asn Leu Ile Val Phe	
65 70 75	
CCT AAC ACT GAT GGT TCG GGT TTT AAT AAA AAA CCA GAA ATA AAA CAC	287
Pro Asn Thr Asp Gly Ser Gly Phe Asn Lys Lys Pro Glu Ile Lys His	
80 85 90 95	
GTT GAA GGT GAT TCT GTT GTG GTT ACT TTT GCA GAA TGT TGT CTT GAC	335
Val Glu Gly Asp Ser Val Val Val Thr Phe Ala Glu Cys Cys Leu Asp	
100 105 110	
TTT AAT AAT TTG ACA GGA AAT CAT CCT CGA AAA TGT GAA AAC TTT TAT	383
Phe Asn Asn Leu Thr Gly Asn His Pro Arg Lys Cys Glu Asn Phe Tyr	
115 120 125	
CCA CTT GTC CCT TCA TTG GGA AAT GCA ATC AAA TTA TGT GAT TGC GTC	431
Pro Leu Val Pro Ser Leu Gly Asn Ala Ile Lys Leu Cys Asp Cys Val	
130 135 140	
ACG GTC CCA CTT TTT TCA CTT CAA GTG ACG TTT TTT CCG GGC TCG GGT	479
Thr Val Pro Leu Phe Ser Leu Gln Val Thr Phe Phe Pro Gly Ser Gly	
145 150 155	

ATA TCA CTA GGA ATG ACG AAT CAT CAT AGC CTT GGT GAC GCT AGC ACG 527  
Ile Ser Leu Gly Met Thr Asn His His Ser Leu Gly Asp Ala Ser Thr  
160 165 170 175  
CGG TTC AAC TTT TTG AAA GGG TGG ACT TCG ATT ATT CAA TCT GGT GTA 575  
Arg Phe Asn Phe Leu Lys Gly Trp Thr Ser Ile Ile Gln Ser Gly Val  
180 185 190  
GAT CGG TCT TTT TTA ACG AAA GGA TCT CCA CCG GTT TTT GAT AGA TTG 623  
Asp Arg Ser Phe Leu Thr Lys Gly Ser Pro Pro Val Phe Asp Arg Leu  
195 200 205  
ATT AAC ATC CCA CAT TTA GAT GAA AAT AAG TTG AGA CAT ACA AGG CTC 671  
Ile Asn Ile Pro His Leu Asp Glu Asn Lys Leu Arg His Thr Arg Leu  
210 215 220  
CAA AGT TTT TAT AAA CCT TCG AGC CTT GTT GGT CCC ACT GAT AAA GTT 719  
Glu Ser Phe Tyr Lys Pro Ser Ser Leu Val Gly Pro Thr Asp Lys Val  
225 230 235  
CGG TCA ACG TTT GTG TTG ACC CGA ACT AAT ATC AAT CTA CTA AAG AAA 767  
Arg Ser Thr Phe Val Leu Thr Arg Thr Asn Ile Asn Leu Leu Lys Lys  
240 245 250 255  
AAG GTC TTA ACC CAA GTG CCA AAC TTG GAG TAC ATG TCA TCT TTT ACG 815  
Lys Val Leu Thr Gln Val Pro Asn Leu Glu Tyr Met Ser Ser Phe Thr  
260 265 270  
GTA ACT TGT GGT TAT ATA TGG AGT TGC ATA GCG AAA TCA CTC GTA AAA 863  
Val Thr Cys Gly Tyr Ile Trp Ser Cys Ile Ala Lys Ser Leu Val Lys  
275 280 285  
ATA GGA GAA AGA AAG GGC GAA GAC GAG TTA GAA CAG TTC ATA ATC ACC 911  
Ile Gly Glu Arg Lys Gly Glu Asp Glu Leu Glu Gln Phe Ile Ile Thr  
290 295 300  
ATT GAT TGT CGA TCT CGT CTT GAT CCA CCA ATT CCC ACA GCC TAC TTT 959  
Ile Asp Cys Arg Ser Arg Leu Asp Pro Pro Ile Pro Thr Ala Tyr Phe  
305 310 315  
GGT AAC TGT GGT GCA CCA TGT GTC CCG ACC TTA AAA AAT GTC GTT TTG 1007  
Gly Asn Cys Gly Ala Pro Cys Val Pro Thr Leu Lys Asn Val Val Leu  
320 325 330 335  
ACT AGC GAA AAT GGG TAT GCA CTT GGT GCT AAA GTA ATT GGA GAG TCT 1055  
Thr Ser Glu Asn Gly Tyr Ala Leu Gly Ala Lys Val Ile Gly Glu Ser  
340 345 350

ATA TGC AAA ATG ATA TAT AAT AAG GAC GGA ATC TTG AAA GAT GCC GCG	1103
Ile Cys Lys Met Ile Tyr Asn Lys Asp Gly Ile Leu Lys Asp Ala Ala	
355 360 365	
AGA TGG CAT GAA CCT TTC ATG ATC CCG GCT AGG AAG ATT GGT GTT GCT	1151
Arg Trp His Glu Pro Phe Met Ile Pro Ala Arg Lys Ile Gly Val Ala	
370 375 380	
GGT ACA CCT AAG CTC AAC TTG TAC GAC TTT GAT TTT GGG TGG GGG AAG	1199
Gly Thr Pro Lys Leu Asn Leu Tyr Asp Phe Asp Phe Gly Trp Gly Lys	
385 390 395	
CCG ATA AAG TAT GAG ACT GTT TCA ATA GAC TAT AAT ACG TCG ATT TCT	1247
Pro Ile Lys Tyr Glu Thr Val Ser Ile Asp Tyr Asn Thr Ser Ile Ser	
400 405 410 415	
ATA AAT GCA AGC AAA ACA TCA GCA CAA GAT CTT GAA ATT GGA TTG AGT	1295
Ile Asn Ala Ser Lys Thr Ser Ala Gln Asp Leu Glu Ile Gly Leu Ser	
420 425 430	
CTA CCG AGT ATG CAA ATG GAG GCG TTT TCT AGC ATC TTT GAT GAA GGA	1343
Leu Pro Ser Met Gln Met Glu Ala Phe Ser Ser Ile Phe Asp Glu Gly	
435 440 445	
TTA GAG AGT CAA GTT TCA TTG TAGATCATCG TCCCCTTTT GTGTGCATCA	1394
Leu Glu Ser Gln Val Ser Leu	
450 454	

AGTTTCTGTC GTTTTATGA GTTGCCACTG TTCTATTCTT TAAGTATACC TTTCGACTAT 1454  
GTTTGAAAGA TGCAACGATA TAAAATGAAA AAAAAAAAAA AAAAAAAAAA AAAA 1508

SEQ ID NO: 6

SEQUENCE LENGTH: 1521

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL SEQUENCE: No

ANTI-SENSE: No

ORIGINAL SOURCE

ORGANISM: Lavandula angustifolia

TISSUE TYPE: petal

IMMEDIATE SOURCE

LIBRARY: cDNA library

CLONE: pLAT21

SEQUENCE DESCRIPTION

-TG ACC ACC CTC CTC GAA TCC TCC CGA GTG GCG CCG CCT CCA GGC ACG 47  
Xxx Thr Thr Leu Leu Glu Ser Ser Arg Val Ala Pro Pro Pro Gly Thr  
1 5 10 15  
GTG GCT GAG CAG TCA CTC CCG CTC ACC TTC TTC GAC ATG ACG TGG CTG 95  
Val Ala Glu Gln Ser Leu Pro Leu Thr Phe Phe Asp Met Thr Trp Leu  
20 25 30  
CAT TTC CAC CCC ATG CTT CAG CTT CTC TTC TAC GAA CTC CCC TGT TCC 143  
His Phe His Pro Met Leu Gln Leu Leu Phe Tyr Glu Leu Pro Cys Ser  
35 40 45  
AAA CCC GCC TTC CTC GAA ACC GTC GTT CCG AAA CTC AAA CAA TCC TTA 191  
Lys Pro Ala Phe Leu Glu Thr Val Val Pro Lys Leu Lys Gln Ser Leu  
50 55 60  
TCT CTA ACC CTC AAA CAC TTC TTC CCC CTT TCA TGC AAT CTA ATC TAC 239  
Ser Leu Thr Leu Lys His Phe Phe Pro Leu Ser Cys Asn Leu Ile Tyr  
65 70 75  
CCT CTA TCG CCG GAG AAA ATG CCG GAG TTC CCG TAT CAG AAC GGT GAC 287  
Pro Leu Ser Pro Glu Lys Met Pro Glu Phe Ser Val Ser Phe Thr Ile  
80 85 90 95  
TCG GTT TCT TTC ACG ATT ATG GAG TCT GTC GGA GAT CAT CCG CAT TCC 335  
Met Glu Ser Ser Asp Asp Tyr Glu Asp Val Gly Asp His Pro His Ser  
100 105 110  
GCT CAT AAA TAC TAC TGC TTT GCC CCT AGC GAC GAT TAT GAA GAT CTC 383  
Ala His Lys Tyr Tyr Cys Phe Ala Gln Leu Pro Pro Ile Val Glu Glu  
115 120 125  
CAG CTG CCG CCG ATA GTC GAG GAA TCT GAT CGG AAA TTG TTT CAA GTT 431  
Ser Asp Arg Lys Leu Phe Gln Val Pro Leu Arg Tyr Gln Asn Gly Asp  
130 135 140  
TTA GCC GTG CAA GTG ACT CTG TTT CCC GGT CGC GGG GTG TGC ATC GGA 479  
Leu Ala Val Gln Val Thr Leu Phe Pro Gly Arg Gly Val Cys Ile Gly  
145 150 155  
ATA ACG ACG CAC CAC ACC GTT AGC GAT GCT CCA TCG TTT GTA GGG TTT 527  
Ile Thr Thr His His Thr Val Ser Asp Ala Pro Ser Phe Val Gly Phe  
160 165 170 175  
ATG AAG AGT TGG GCT TCC ATC ACT AAA TTC GGA GGA GAT GAT GAA TTC 575  
Met Lys Ser Trp Ala Ser Ile Thr Lys Phe Gly Gly Asp Asp Glu Phe  
180 185 190

TTG GAC GGA AAA GGT GAA TGT TTG CCG GTT TTC GAC CGA TCG CTC CTG 623  
Leu Asp Gly Lys Gly Glu Cys Leu Pro Val Phe Asp Arg Ser Leu Val  
195 200 205  
AAT TAT CCG CCT AAA TTG GAC ACA TAT TTA TGG AAC AAC GCC CAG AAA 671  
Asn Tyr Pro Pro Lys Leu Asp Thr Tyr Leu Trp Asn Asn Ala Gln Lys  
210 215 220  
CGT CCG TTG GAA TCG CAG CAT CCA TCT TTA CCG ACG GAT CGG ATT CGA 719  
Arg Pro Leu Glu Ser Gln His Pro Ser Leu Pro Thr Asp Arg Ile Arg  
225 230 235  
GCT ACC TAC CTT TTC ACC CAA TCT GAA ATT AAG AAA TTG AAG GGT TTG 767  
Ala Thr Tyr Leu Phe Thr Gln Ser Glu Ile Lys Lys Leu Lys Gly Leu  
240 245 250 255  
ATT CAG AGA AAA GCC CCA AAT GTA GTT AAT CTC TCT TCC TTC GTC GCG 815  
Ile Gln Arg Lys Ala Pro Asn Val Val Asn Leu Ser Ser Phe Val Ala  
260 265 270  
ATC GCA GCT TAT ATC TGG ACC GGC ATC GCC AAA TCG GTC GGA GAT TAC 863  
Ile Ala Ala Tyr Ile Trp Thr Gly Ile Ala Lys Ser Val Gly Asp Tyr  
275 280 285  
AAA GAC GTG GAT GAC GAC AAA CGC GCT TTC TTT TTA ATT CCG ATC GAT 911  
Lys Asp Val Asp Asp Lys Arg Ala Phe Phe Leu Ile Pro Ile Asp  
290 295 300  
TTA AGG CCG CGT TTG GAT CCG CCG GCT CCG GGG AAC TAC TTC GGA AAC 959  
Leu Arg Pro Arg Leu Asp Pro Pro Ala Pro Gly Asn Tyr Phe Gly Asn  
305 310 315  
TGT CTA TCG TTT GCG ATG GCG AAG ATC CTG CGG CGG GAT TTG GTC GGA 1007  
Cys Leu Ser Phe Ala Met Ala Lys Ile Leu Arg Arg Asp Leu Val Gly  
320 325 330 335  
GAT GAA GGG GTG TTT CCG GCA GCT GAG GCG ATC GCG GCG GAA ATA GAG 1055  
Asp Glu Gly Val Phe Arg Ala Ala Glu Ala Ile Ala Ala Glu Ile Glu  
340 345 350  
AAG AGG ACG AGC GAC AAG AAG ATT CTA GAA ACT GTG GAG AAC TGG CCG 1103  
Lys Arg Thr Ser Asp Lys Lys Ile Leu Glu Thr Val Glu Asn Trp Pro  
355 360 365  
TCT GAG ATT CGC GAA GCC TTG CAA AAC TGT TAT TTC TCG GTG GCG GGA 1151  
Ser Glu Ile Arg Glu Ala Leu Gln Asn Cys Tyr Phe Ser Val Ala Gly  
370 375 380

TCG AGC AGG CTT GAT CTT TAC GGC GCG GAT TTT GGA TGG GGT AAG GCG 1199  
Ser Ser Arg Leu Asp Leu Tyr Gly Ala Asp Phe Gly Trp Gly Lys Ala  
385 390 395  
GTG AAG CAA GAG ATA CTG TCG ATT GAT GGA GAG AAG TTT ACG ATG TCG 1247  
Val Lys Gln Glu Ile Leu Ser Ile Asp Gly Glu Lys Phe Thr Met Ser  
400 405 410 415  
TTG TGT AAA CCG AGG GAT GCT GCC GGA GGA TTG GAG GTT GGA TTG TCT 1295  
Leu Cys Lys Pro Arg Asp Ala Ala Gly Gly Leu Glu Val Gly Leu Ser  
420 425 430  
TTG CCA AAG GAG GAA TTG CAA GCT TTT GAT GAT TAT TTT GCG GAG GGA 1343  
Leu Pro Lys Glu Glu Leu Gln Ala Phe Asp Asp Tyr Phe Ala Glu Gly  
435 440 445  
ATA AAG GGT TGATTAATCA TTTAATCATG TATTATGAAG TTGGATGAAA 1392  
Ile Lys Gly  
450  
TCCTCTGTTT CATCTCTATT GTTTAAACAA TAATTTTTT CCATTGAAC TTTTGAGTC 1452  
AATAAAAAAA AAAAAAAA AAAAAAAATG AAAAAACTCA GTTATTTTTT TTTTTTTTT 1512  
TTTTTTTT  
1521

SEQ ID NO: 7

SEQUENCE LENGTH: 10

SEQUENCE TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL SEQUENCE: No

SEQUENCE DESCRIPTION

Arg Phe Leu Gly Ile Thr Gly Ser Pro Lys

1

5

10

SEQ ID NO: 8

SEQUENCE LENGTH: 8

SEQUENCE TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL SEQUENCE: No

SEQUENCE DESCRIPTION

Ile His Met Asp Ala Phe Ala Lys

1

5

SEQ ID NO: 9

SEQUENCE LENGTH: 10

SEQUENCE TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL SEQUENCE: No

SEQUENCE DESCRIPTION

Gly Val Glu Ile Gly Val Ser Leu Pro Lys

1 5 10

SEQ ID NO: 10

SEQUENCE LENGTH: 8

SEQUENCE TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL SEQUENCE: No

SEQUENCE DESCRIPTION

Ala Ser Leu Ser Leu Thr Leu Lys

1 5

SEQ ID NO: 11

SEQUENCE LENGTH: 14

SEQUENCE TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL SEQUENCE: No

SEQUENCE DESCRIPTION

His Tyr Val Pro Leu Ser Gly Asn Leu Leu Met Pro Ile Lys

1 5 10

SEQ ID NO: 12

SEQUENCE LENGTH: 14

SEQUENCE TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL SEQUENCE: No

SEQUENCE DESCRIPTION

Val Arg Ala Thr Tyr Val Leu Ser Leu Ala Glu Ile Gln Lys

1 5 10

SEQ ID NO: 13

SEQUENCE LENGTH: 8

SEQUENCE TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL SEQUENCE: No

SEQUENCE DESCRIPTION

Ile His Met Asp Ala Phe Ala Lys

1 5

SEQ ID NO: 14

SEQUENCE LENGTH: 9

SEQUENCE TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL SEQUENCE: No

SEQUENCE DESCRIPTION

Lys Ile His Met Asp Ala Phe Ala Lys

1 5

SEQ ID NO: 15

SEQUENCE LENGTH: 8

SEQUENCE TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL SEQUENCE: No

SEQUENCE DESCRIPTION

Lys Ile His Met Asp Ala Phe Ala

1 5

SEQ ID NO: 16

SEQUENCE LENGTH: 23

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: synthetic DNA

HYPOTHETICAL SEQUENCE: No

SEQUENCE DESCRIPTION

AARATHCAYA TGGAYGCITT YGC

SEQ ID NO: 17

SEQUENCE LENGTH: 23

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: synthetic DNA

HYPOTHETICAL SEQUENCE: No

SEQUENCE DESCRIPTION

CTCGAGTTTT TTTTTTTTT TTT

23

SEQ ID NO: 18

SEQUENCE LENGTH: 26

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: synthetic DNA

HYPOTHETICAL SEQUENCE: No

SEQUENCE DESCRIPTION

TTCACCATGG AGCAAATCCA AATGGT

26

SEQ ID NO: 19

SEQUENCE LENGTH: 17

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: synthetic DNA

HYPOTHETICAL SEQUENCE: No

SEQUENCE DESCRIPTION

CGAGTCGCC CTCATCAC

17

SEQ ID NO: 20

SEQUENCE LENGTH: 16

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: synthetic DNA

HYPOTHETICAL SEQUENCE: No

SEQUENCE DESCRIPTION

AACAGCTATG ACCATG

16

SEQ ID NO: 21

SEQUENCE LENGTH: 6

SEQUENCE TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide  
HYPOTHETICAL SEQUENCE: No  
SEQUENCE DESCRIPTION  
Asp Phe Gly Trp Gly Lys  
1 5  
SEQ ID NO: 22  
SEQUENCE LENGTH: 17  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: synthetic DNA  
HYPOTHETICAL SEQUENCE: No  
SEQUENCE DESCRIPTION  
GAYTTYG GIT GGGGIAA 17  
SEQ ID NO: 23  
SEQUENCE LENGTH: 21  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: synthetic DNA  
HYPOTHETICAL SEQUENCE: No  
SEQUENCE DESCRIPTION  
TGGCAACTGT CTTCCGTCAT G 21  
SEQ ID NO: 24  
SEQUENCE LENGTH: 23  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: synthetic DNA  
HYPOTHETICAL SEQUENCE: No  
SEQUENCE DESCRIPTION  
CCATGTCAGG TGTGAGGTTC AAC 23  
SEQ ID NO: 25  
SEQUENCE LENGTH: 20  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: synthetic DNA

HYPOTHETICAL SEQUENCE: No

SEQUENCE DESCRIPTION

ATCGTTTCGC ATGATTGAAC

20

SEQ ID NO: 26

SEQUENCE LENGTH: 20

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: synthetic DNA

HYPOTHETICAL SEQUENCE: No

SEQUENCE DESCRIPTION

TCAGAAAGAAC TCGTCAAGAA

20

SEQ ID NO: 27

SEQUENCE LENGTH: 53

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: synthetic DNA

HYPOTHETICAL SEQUENCE: No

SEQUENCE DESCRIPTION

GGGATCCAAC A ATG GAG CAA ATC CAA ATG GTG GCC GTG ATC GAA ACG TGT

50

Met Glu Gln Ile Gln Met Val Ala Val Ile Glu Thr Cys

1

5

10

AGA

53

Arg

15

SEQ ID NO: 28

SEQUENCE LENGTH: 16

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: synthetic DNA

HYPOTHETICAL SEQUENCE: No

SEQUENCE DESCRIPTION

GTAAAACGAC GGCCAT

16

SEQ ID NO: 29

SEQUENCE LENGTH: 45

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: synthetic DNA

HYPOTHETICAL SEQUENCE: No

SEQUENCE DESCRIPTION

GGGATCCAAC A ATG GAG CAA ATC CAA ATG GTG AAC ATT CTC GAA C

45

Met Glu Gln Ile Gln Met Val Asn Ile Leu Glu

1

5

10

SEQ ID NO: 30

SEQUENCE LENGTH: 21

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: synthetic DNA

HYPOTHETICAL SEQUENCE: No

SEQUENCE DESCRIPTION

CTCGGAGGAA TTCGGCACGA C

21

SEQ ID NO: 31

SEQUENCE LENGTH: 35

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: synthetic DNA

HYPOTHETICAL SEQUENCE: No

SEQUENCE DESCRIPTION

AGTCGGATCC AACAA ATG ACC ACC CTC CTC GAA TCC

35

Thr Thr Leu Leu Glu Ser

1

5